

Figure 1

85P1B3 SSH sequence and GenBank homology to OIP5

GATCAGAGGACACATGGGACTCTGCATCTTAATTCCTAAATTTACAGTCAAAGACATTTTCAG
AGATAAGTATTATGAATTCAATAAGAATCTAAAGTAAGTTCTTAAGGCAAATAGCTATAAAA
GAGAAGAATCCTTAGTCTCTCATCTTCTAAAAACAGCTTCACAAATAATTTGGAAAATCAGCC
TAAAGGTAAATAGAACTGCATTTCCCTCCATTCTTGAAGCCAATCTTTTCAAGAAATGAC
TAAGCAGCACCTGTTGTTGAAGACAGCAATAAAGCCTGAACCTGACACTCAAGCTTTGGTACA
GGATC

gb|AF025441.1|AF025441 Homo sapiens Opa-interacting protein... 632 e-179
gb|AF158642.1|AF158642 Homo sapiens metalloproteinase-disin... 42 0.12
gb|AC005075.2|AC005075 Homo sapiens clone RG219E16, complet... 42 0.12
emb|AL096773.6|HS1000E10 Human DNA sequence from clone 1000... 40 0.48

>gb|AF025441.1|AF025441 Homo sapiens Opa-interacting protein OIP5 mRNA, partial cds
Length = 1197

Score = 632 bits (319), Expect = e-179
Identities = 319/319 (100%)
Strand = Plus / Minus

Query: 1 gatcagaggacacatgggactctgcatcttaattcctaaatttacagtcaaagacat ttt 60
|||||
Sbjct: 1013 gatcagaggacacatgggactctgcatcttaattcctaaatttacagtcaaagacat ttt 954

Query: 61 cagagataagtattatgaattcaataagaatctaaagtaagttcttaaggcaaatagcta 120
|||||
Sbjct: 953 cagagataagtattatgaattcaataagaatctaaagtaagttcttaaggcaaatagcta 894

Query: 121 taaaagagaagaatccttagtctctcatcttctaaaaacagcttcacaaataatttgga 180
|||||
Sbjct: 893 taaaagagaagaatccttagtctctcatcttctaaaaacagcttcacaaataatttgga 834

Query: 181 aatcagcctaaaggtaaatagaaactgcatttccctccattcttgaagccaatctttt 240
|||||
Sbjct: 833 aatcagcctaaaggtaaatagaaactgcatttccctccattcttgaagccaatctttt 774

Query: 241 caagaaatgactaagcagcacctgttggtgaagacagcaataaagcctgaacctgacact 300
|||||
Sbjct: 773 caagaaatgactaagcagcacctgttggtgaagacagcaataaagcctgaacctgacact 714

Query: 301 caagctttggtacaggatc 319
|||||
Sbjct: 713 caagctttggtacaggatc 695

5'	GGC	TGC	GGG	AAG	ATG	GCG	GCT	CAG	CCG	CTG	CGG	CAT	CGC	TCA	CGT	TGT	GCA	ACG	54
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				M		A	A	Q	P	L	R	H	R	S	R	C	A	T	
			63			72			81			90			99			108	
CCG	CCC	CGG	GGG	GAC	TTT	TGT	GGT	GGC	ACT	GAG	AGG	GCG	ATT	GAC	CAA	GCT	TCT		
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
P	P	R	G	D	F	C	G	G	T	E	R	A	I	D	Q	A	S		
			117			126			135			144			153			162	
TTT	ACG	ACC	TCC	ATG	GAG	TGG	GAT	ACG	CAG	GTG	GTG	AAG	GGG	TCC	TCG	CCG	CTC		
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F	T	T	S	M	E	W	D	T	Q	V	V	K	G	S	S	P	L		
			171			180			189			198			207			216	
GGC	CCC	GCA	GGG	CTG	GGG	GCT	GAG	GAG	CCA	GCC	GCC	GGC	CCG	CAG	CTG	CCG	TCT		
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
G	P	A	G	L	G	A	E	E	P	A	A	G	P	Q	L	P	S		
			225			234			243			252			261			270	
TGG	CTG	CAG	CCT	GAG	AGG	TGC	GCT	GTG	TTC	CAG	TGC	GCA	CAG	TGT	CAC	GCA	GTG		
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
W	L	Q	P	E	R	C	A	V	F	Q	C	A	Q	C	H	A	V		
			279			288			297			306			315			324	
CTC	GCC	GAC	TCG	GTG	CAC	CTC	GCC	TGG	GAC	CTG	TCG	CGG	TCC	CTC	GGG	GCC	GTG		
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L	A	D	S	V	H	L	A	W	D	L	S	R	S	L	G	A	V		
			333			342			351			360			369			378	
GTC	TTC	TCC	AGA	GTT	ACA	AAT	AAC	GTC	GTT	TTG	GAA	GCG	CCC	TTC	CTA	GTT	GGC		
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
V	F	S	R	V	T	N	N	V	V	L	E	A	P	F	L	V	G		
			387			396			405			414			423			432	
ATT	GAA	GGT	TCA	CTC	AAA	GGC	AGT	ACT	TAC	AAC	CTT	TTA	TTC	TGT	GGT	TCT	TGT		
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
I	E	G	S	L	K	G	S	T	Y	N	L	L	F	C	G	S	C		
			441			450			459			468			477			486	
GGG	ATT	CCC	GTT	GGT	TTC	CAT	CTG	TAT	TCT	ACC	CAT	GCT	GCC	CTG	GCT	GCC	TTG		
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
G	I	P	V	G	F	H	L	Y	S	T	H	A	A	L	A	A	L		
			495			504			513			522			531			540	
AGA	GGT	CAC	TTC	TGC	CTT														

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657			666			675			684			693			702		
CTA	ATG	AAG	ATT	CTG	AGT	GAA	GTG	ACT	CCT	GAC	CAG	TCC	AAG	CCA	GAA	AAC	TGA
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L	M	K	I	L	S	E	V	T	P	D	Q	S	K	P	E	N	*
711			720			729			738			747			756		
TCC	TGT	ACC	AAA	GCT	TGA	GTG	TCA	GGT	TCA	GGC	TTT	ATT	GCT	GTC	TTC	AAC	AAC
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
765			774			783			792			801			810		
AGG	TGC	TGC	TTA	GTC	ATT	TCT	TGA	AAA	AGA	TTG	GCT	TCA	AGA	ATG	GAG	GGG	AAA
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
819			828			837			846			855			864		
TGC	AGT	TTC	TAT	TTA	CCT	TTA	GGC	TGA	TTT	TCC	AAA	TTA	TTT	GTG	AAG	CTG	TTT
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
873			882			891			900			909			918		
TTA	GAA	GAT	GAG	AGA	CTA	AGG	ATT	CTT	CTC	TTT	TAT	AGC	TAT	TTG	CCT	TAA	GAA
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
927			936			945			954			963			972		
CTT	ACT	TTA	GAT	TCT	TAT	TGA	ATT	CAT	AAT	ACT	TAT	CTC	TGA	AAA	TGT	CTT	TGA
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981			990			999			1008			1017			1026		
CTG	TAA	ATT	TAG	GAA	TTA	AGA	TGC	AGA	GTC	CCA	TGT	GTC	CTC	TGA	TCT	AAA	GTT
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
1035			1044			1053			1062			1071			1080		
GCA	TGG	TTG	GTC	TGA	AAA	TAG	AGT	TGG	GCT	TAA	TGT	TGA	CTT	CTA	TTA	CTC	CTG
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
1089			1098			1107			1116			1125			1134		
CAT	GGA	GCA	GTT	GTT	ATG	AAT	ACT	AAT	ACA	TCA	CTT	TTT	AAC	TTC	TGT	AAA	ATA
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
1143			1152			1161			1170			1179			1188		
CAG	ATC	ATA	ATA	TTC	TAT	AGG	TAA	TGT	TTA	ATA	AAT	TGC	CTG	AAT	AAT	AAA	AAA
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
1197			1206			1215			1224			1233			1242		
AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA
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1251			1260														
AAA	AAA	AAA	AAA	AAA	AAA	AA	3'										

Pub. No. 5,115,820

85P1B3/OIP5 protein sequence.

1 MAAQPLRHRS RCATPPRGDF CGGTERAIDQ ASFTTSMEDW TQVVKGS SPL GPAGLGAEEP
61 AAGPQLPSWL QPERCAVFQC AQCHAVLADS VHLLAWDLRS LGAVVFSRVT NNVVLEAPFL
121 VGIEGSLKGS TYNLLFCGSC GIPVGPHLYS THAALAALRG HFCLSSDKMV CYLLKTKAIV
181 NASEMDIQNV PLSEKIAELK EKIVLTHNRL KSLMKILSEV TPDQSKPEN*

Alignment of 85P1B3 with OIP5.

85P1B3:	1	MAAQPLRHRSRCATPPRGDFCGGTERAIDQASFTTSMEDWTQVVKGSSPLGPAGLGAEEP	60
		MAAQPLRHRSRCATPPRGDFCGGTERAIDQASFTTSMEDWTQVVKGSSPLGPAGLGAEEP	
OIP5:	3	MAAQPLRHRSRCATPPRGDFCGGTERAIDQASFTTSMEDWTQVVKGSSPLGPAGLGAEEP	62
85P1B3:	61	AAGPQLPSWLQPERCAVFCQAQCHAVLADSVHLAWDLRSRLGAVVFSRVTTNNVVLEAPFL	120
		AAGPQLPSWLQPERCAVFCQAQCHAVLADSVHLAWDLRSRLGAVVFSRVTTNNVVLEAPFL	
OIP5:	63	AAGPQLPSWLQPERCAVFCQAQCHAVLADSVHLAWDLRSRLGAVVFSRVTTNNVVLEAPFL	122
85P1B3:	121	VGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALALRGHFCLSSDKMVCYLLKTKAIV	180
		VGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALALRGHFCLSSDKMVCYLLKTKAIV	
OIP5:	123	VGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALALRGHFCLSSDKMVCYLLKTKAIV	182
85P1B3:	181	NASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLMKILSEVTPDQSKPEN	229
		NASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLMKILSEVTPDQSKPEN	
OIP5:	183	NASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLMKILSEVTPDQSKPEN	231

Figure 5: 85P1B3 Hydrophilicity profile
(Hopp T.P., Woods K.R., 1981. Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

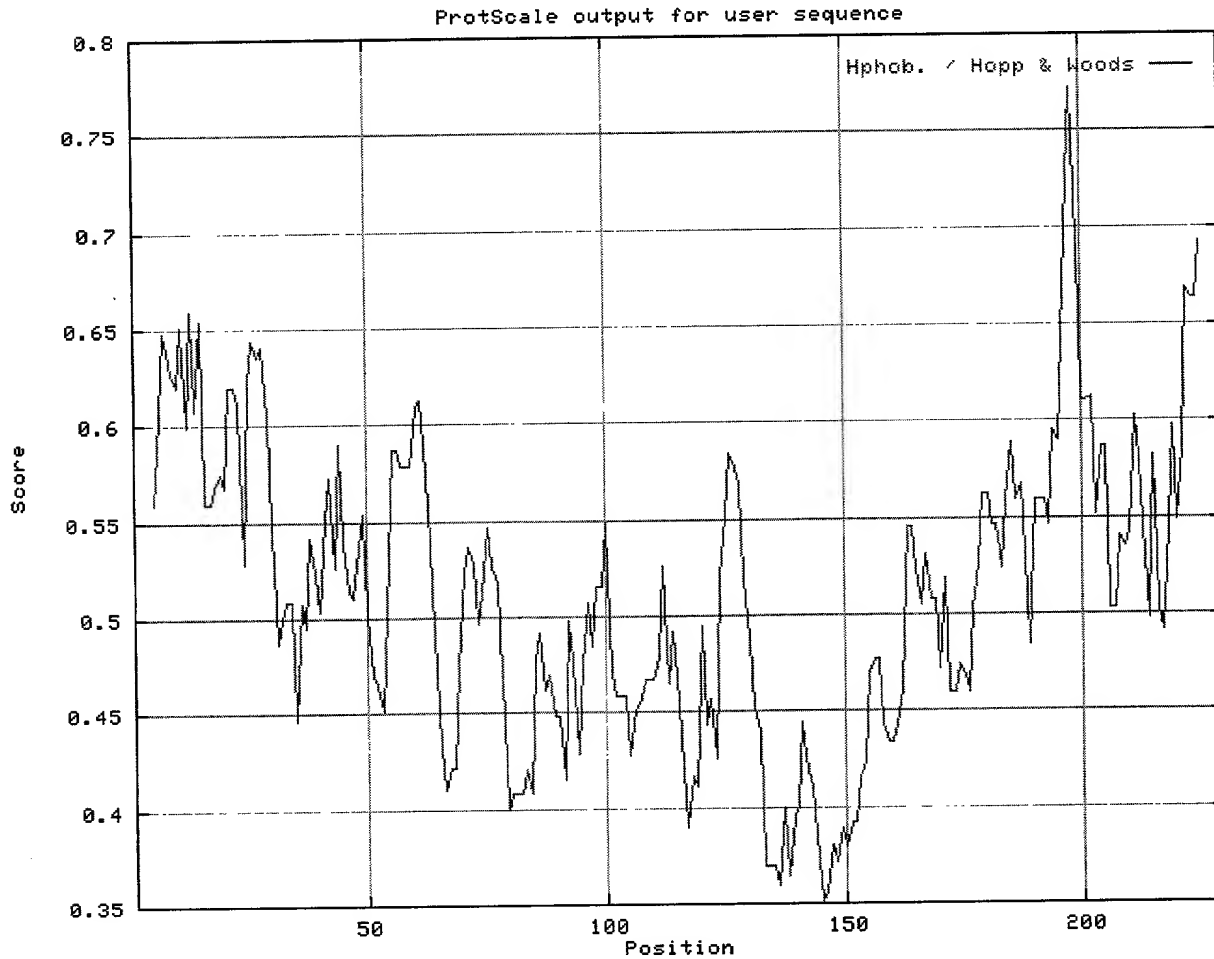


Figure 6: 85P1B3 Hydropathicity Profile
(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

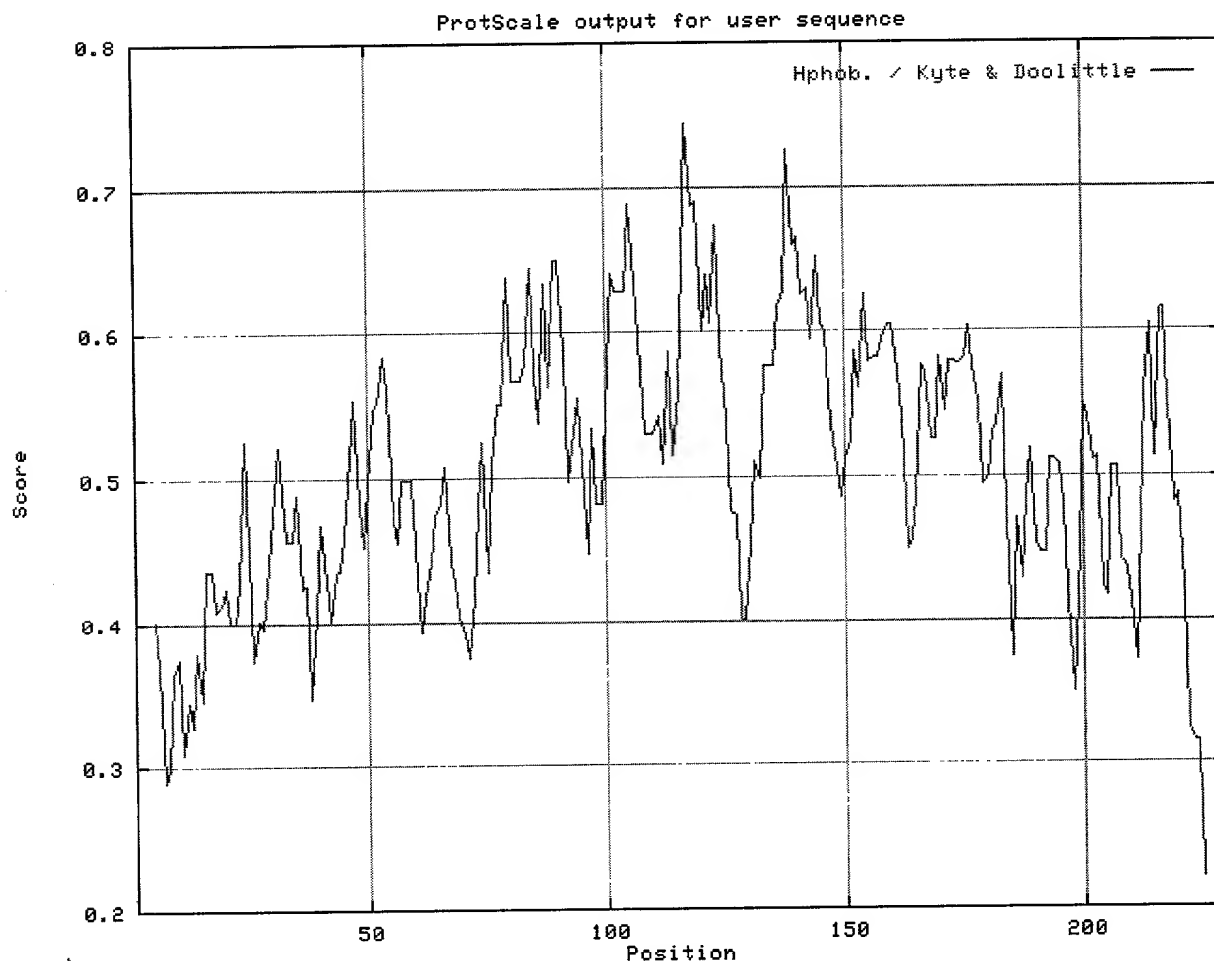


Figure 7: 85P1B3 % Accessible Residues Profile
(Janin J., 1979. Nature 277:491-492)

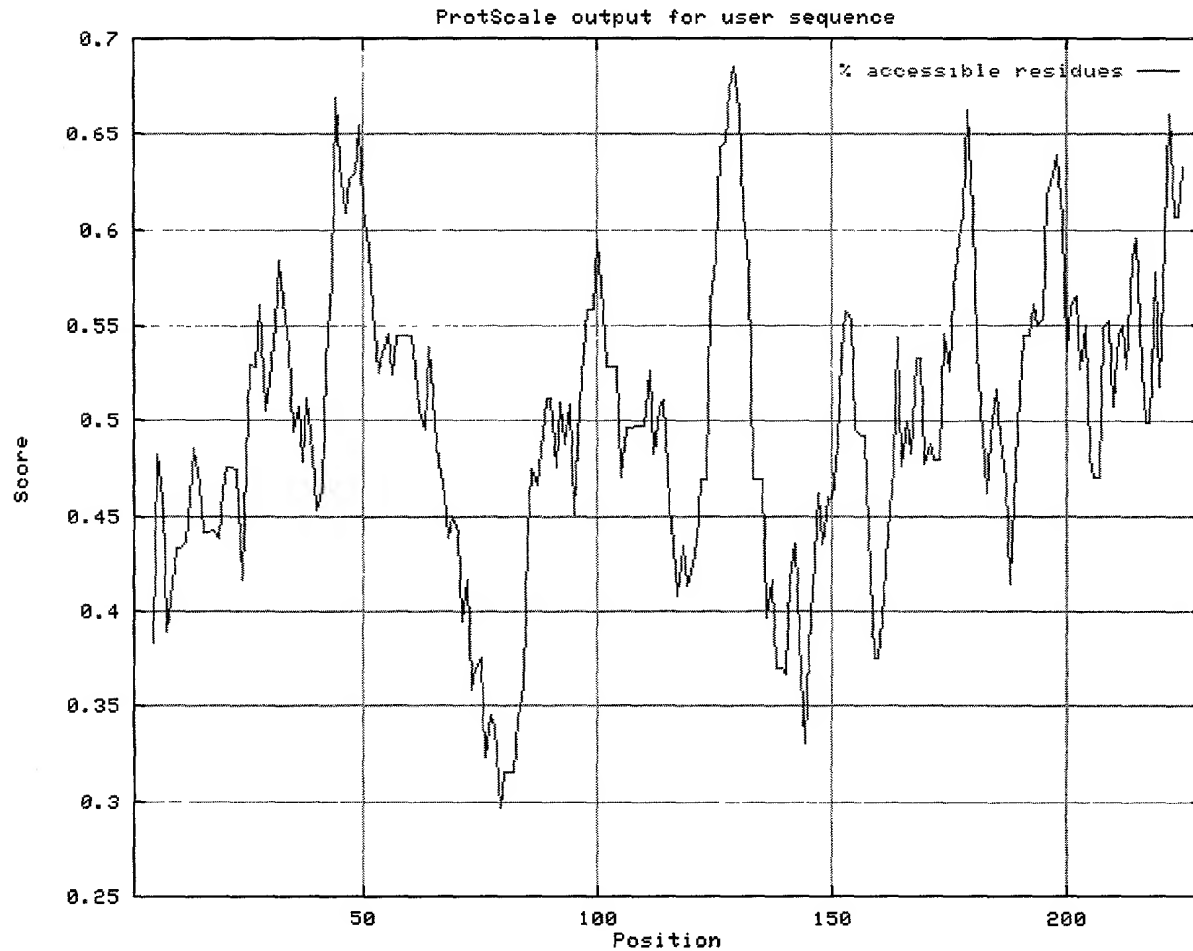


Figure 8: 85P1B3 Average Flexibility Profile

(Bhaskaran R., Ponnuswamy P.K., 1988.

Int. J. Pept. Protein Res. 32:242-255)

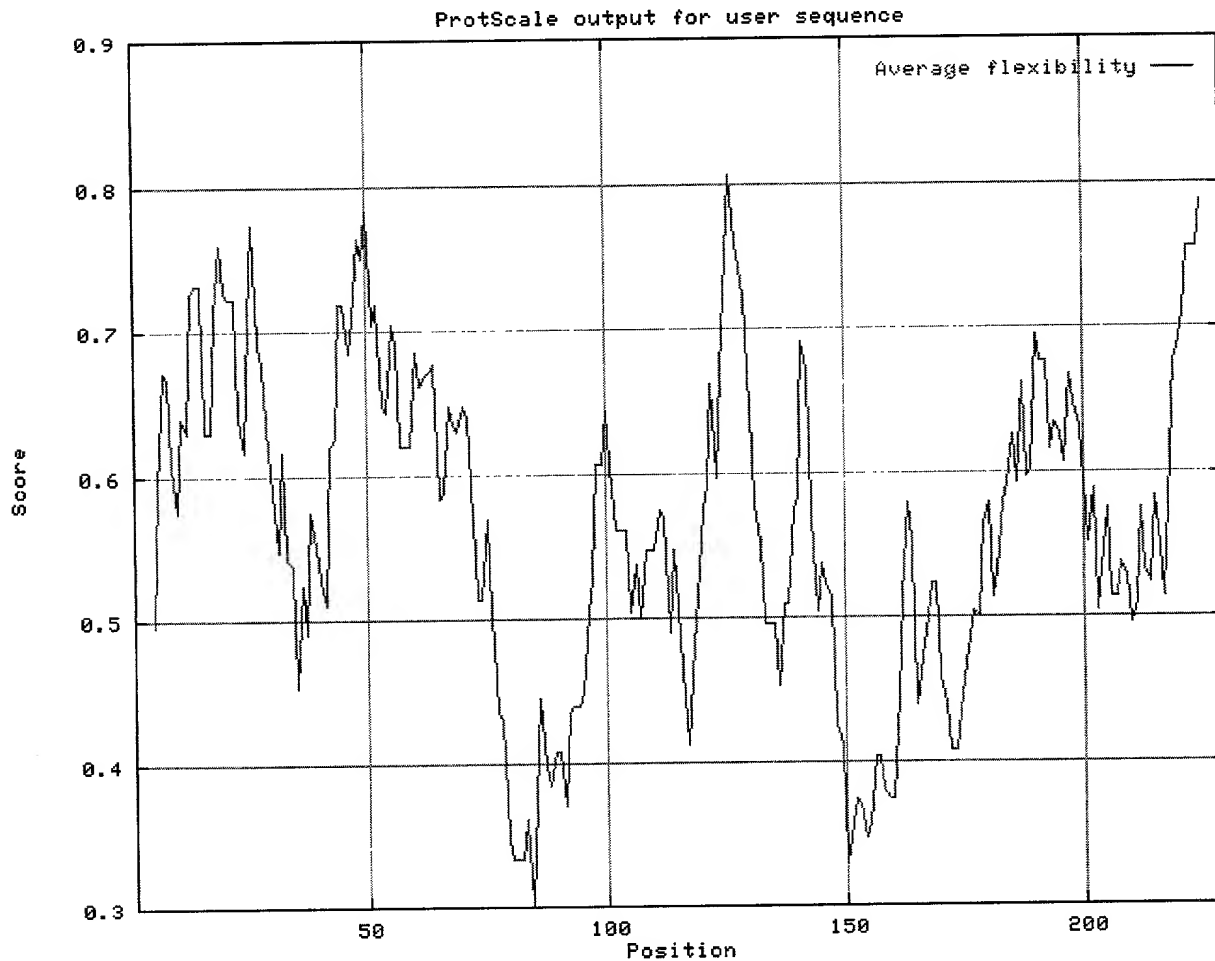


Figure 9: 85P1B3 Beta-turn Profile
(Deleage, G., Roux B. 1987. Protein Engineering 1:289-294)

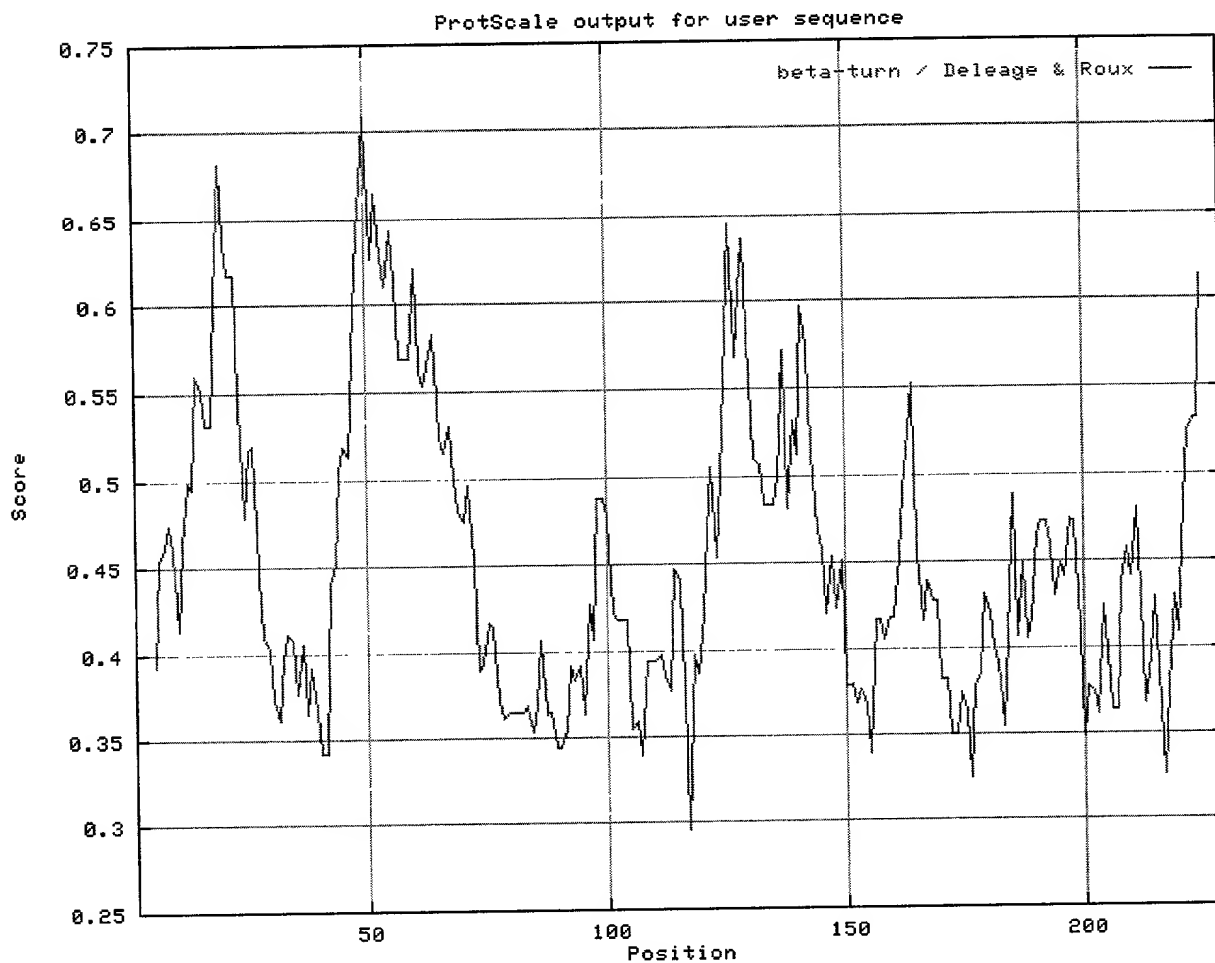


Figure 10 RT-PCR analysis of 85P1B3 expression.

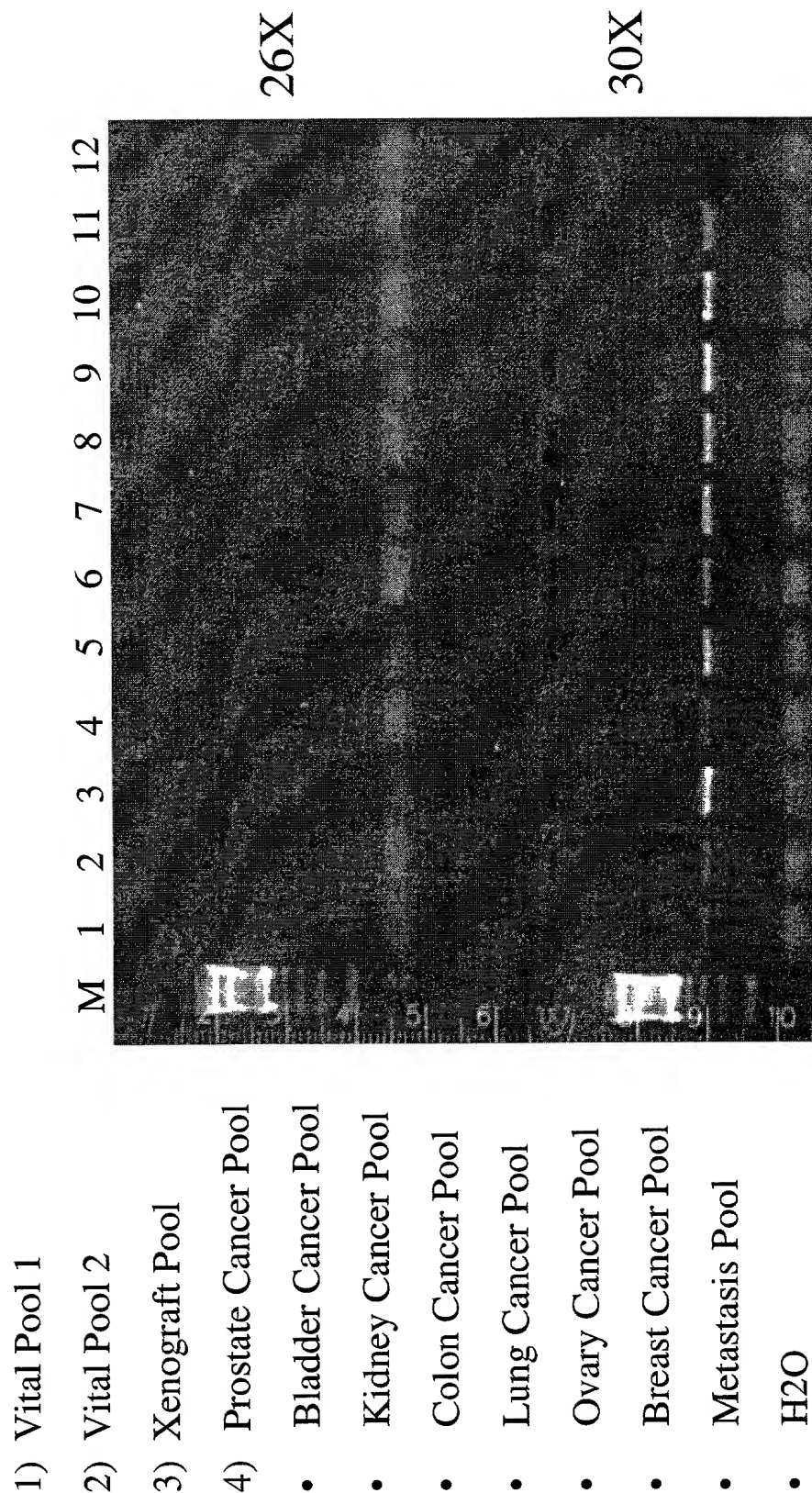


Figure 11 Expression of 85P1B3 in Normal Human Tissues

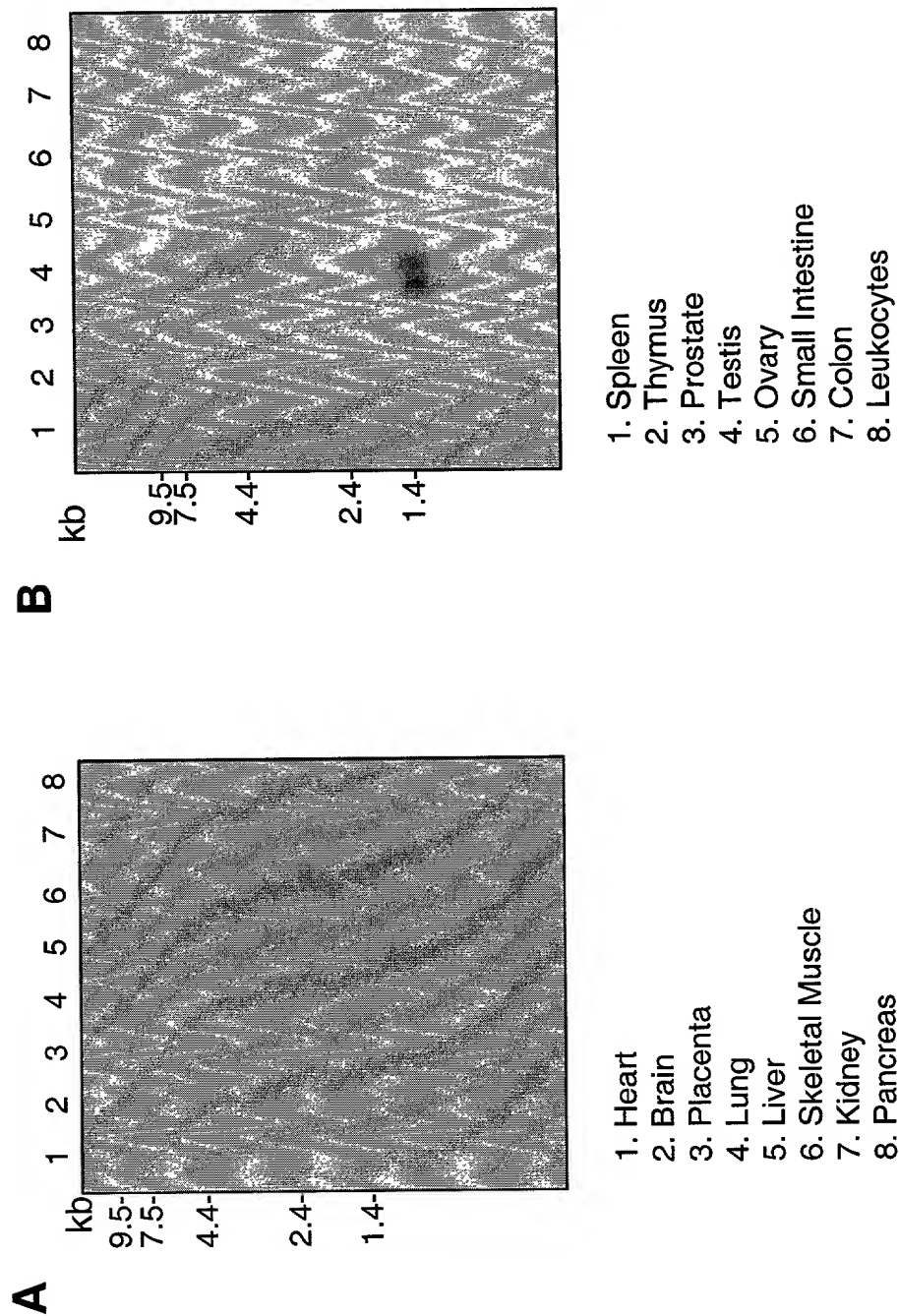


Figure 12 Expression of 85P1B3 in Human Cancer Cell lines

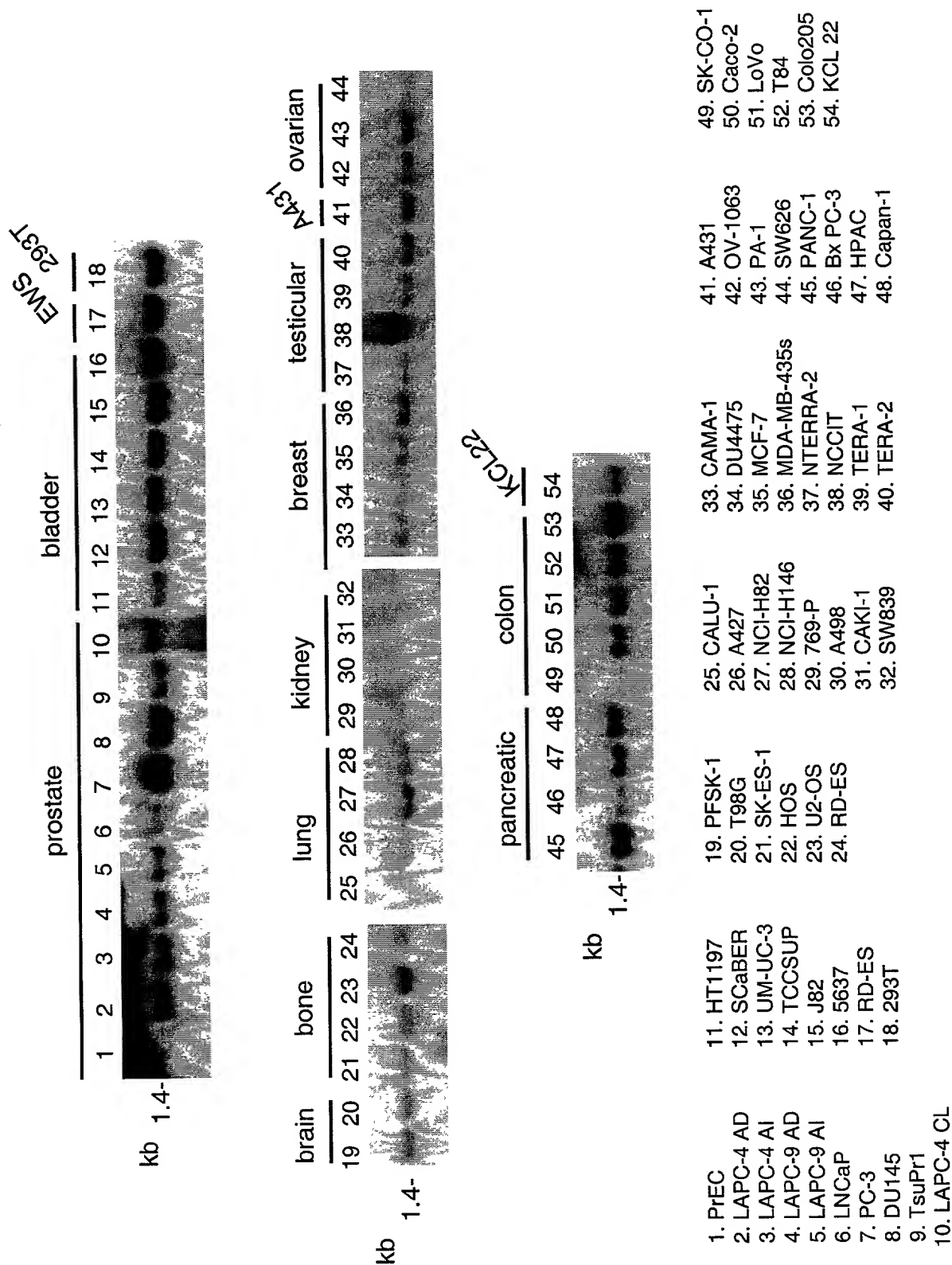
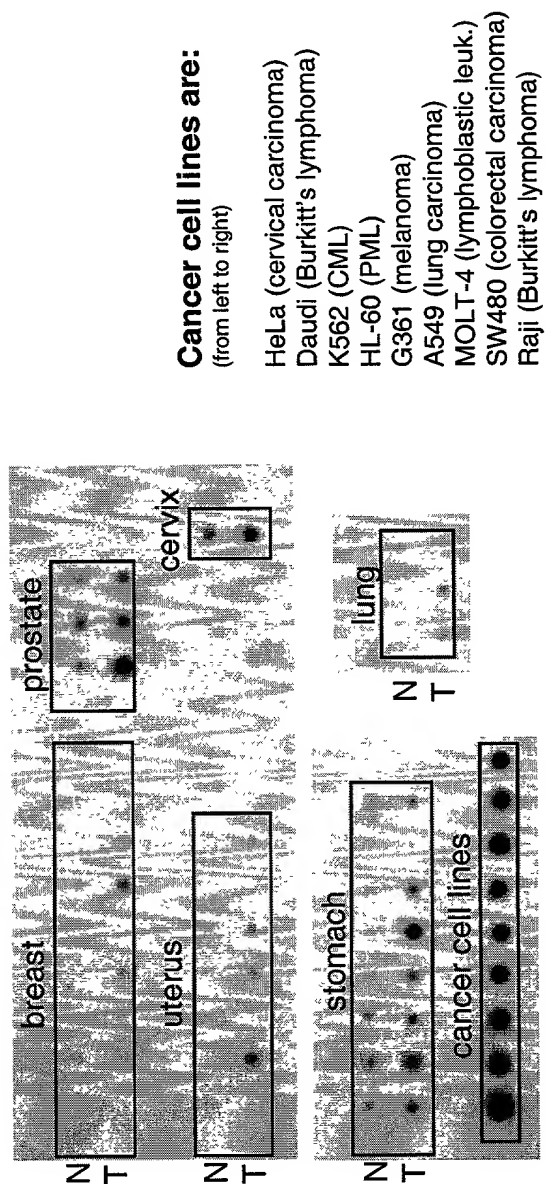


Figure 13 Expression of 85P1B3 in Patient Cancer Specimens and Cancer Cell Lines



T = tumor RNA
N = normal adjacent tissue RNA

P1 – Stage III, T2N1MX
P2 – Stage III, T3N1MX

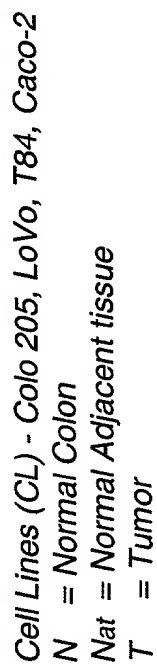


Figure 15 Expression of 85P1B3 in Bladder Cancer Patient Specimens

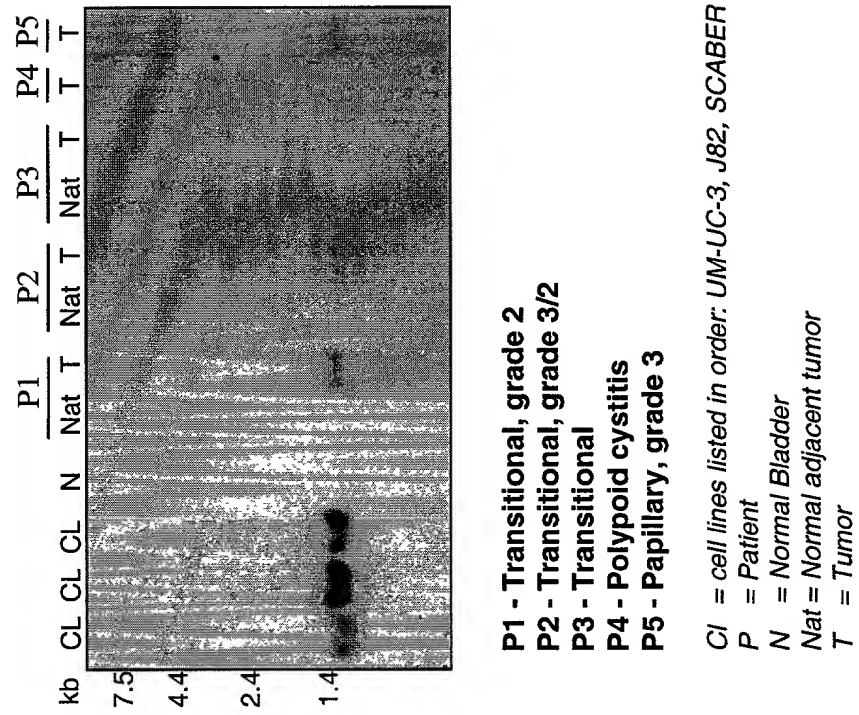


Figure 16 Expression of 85P1B3 in Lung Cancer Patient Specimens

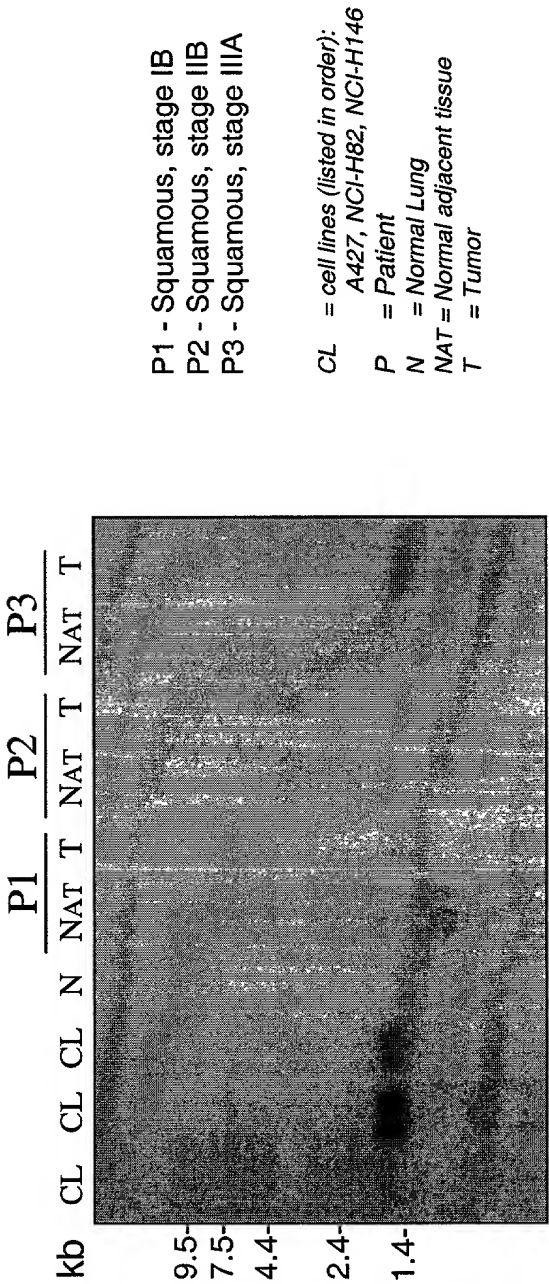


Figure 17 Expression of 85P1B3 in Prostate Cancer Xenografts Following

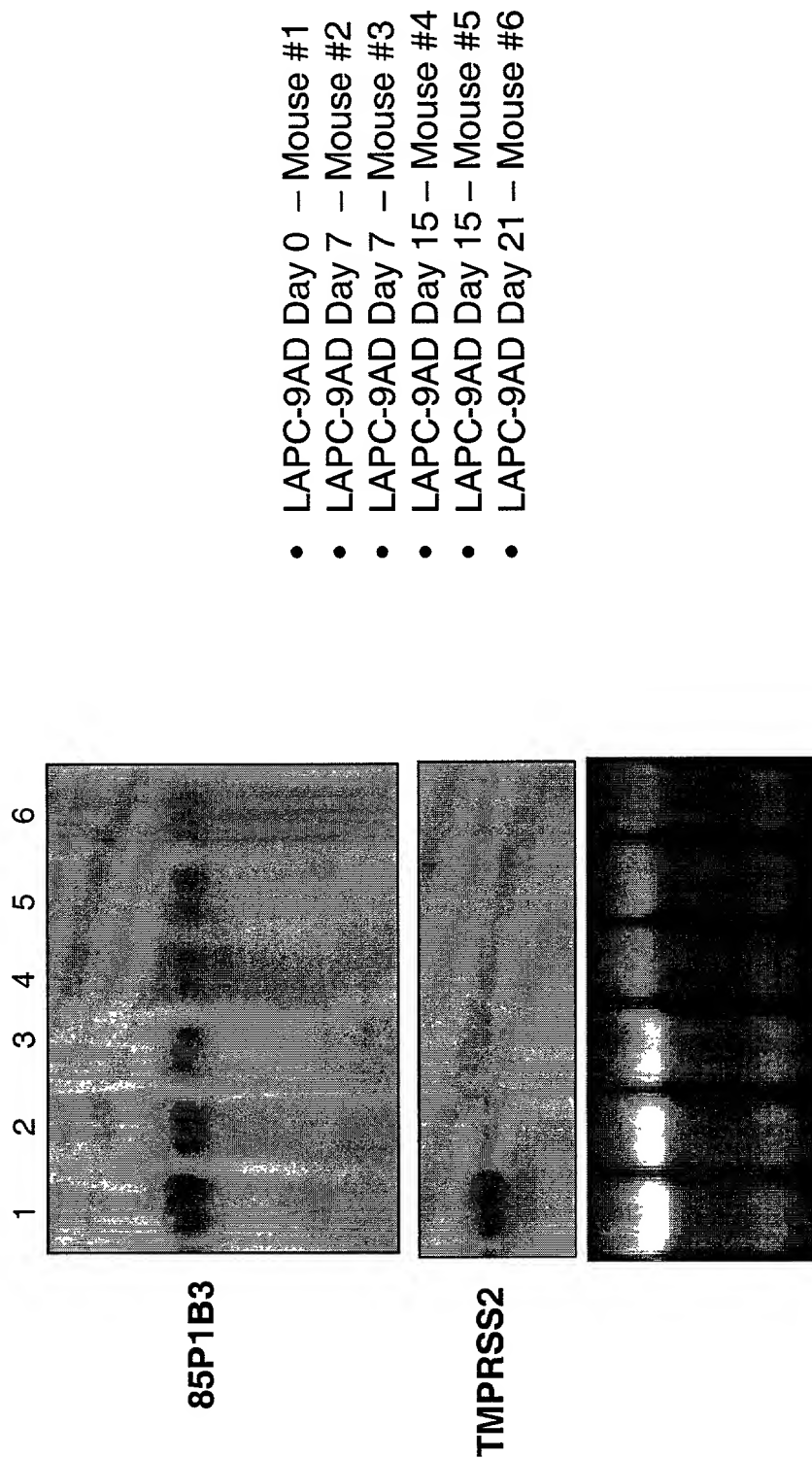


Figure 18 Expression of 85P1B3 in PC3 Cells Following Retroviral-Mediated Gene Delivery

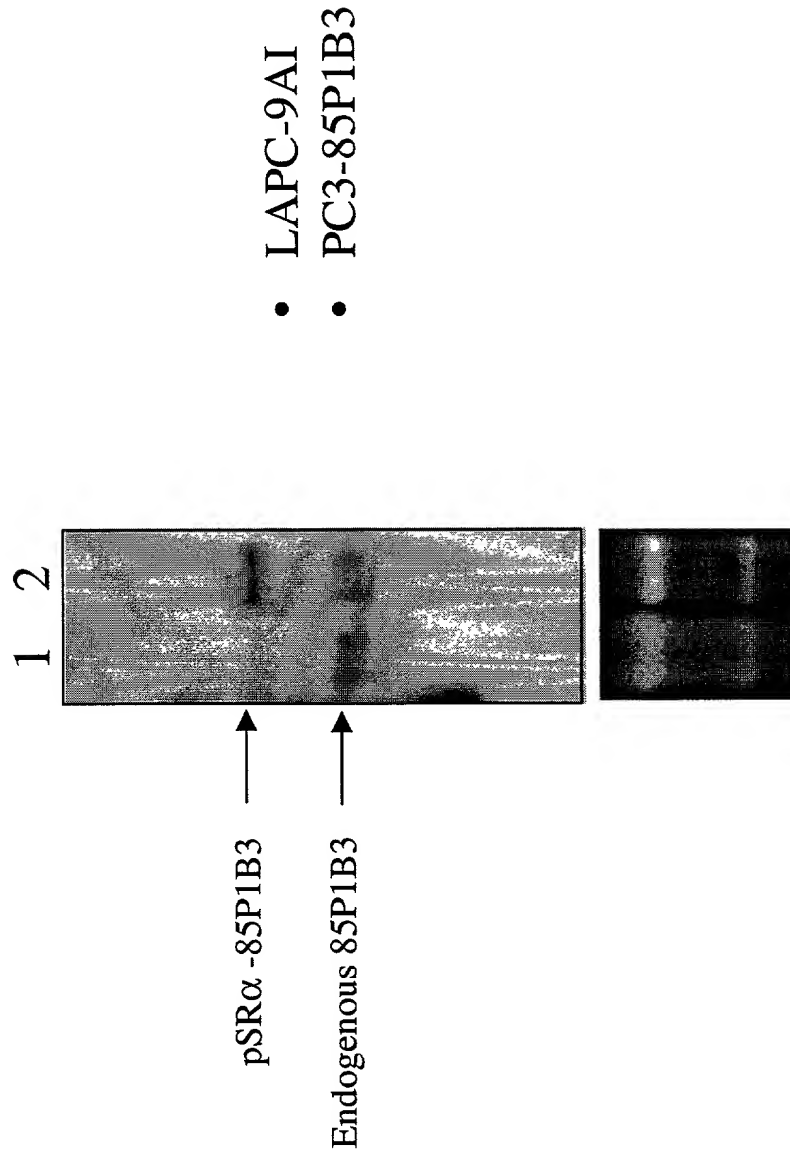
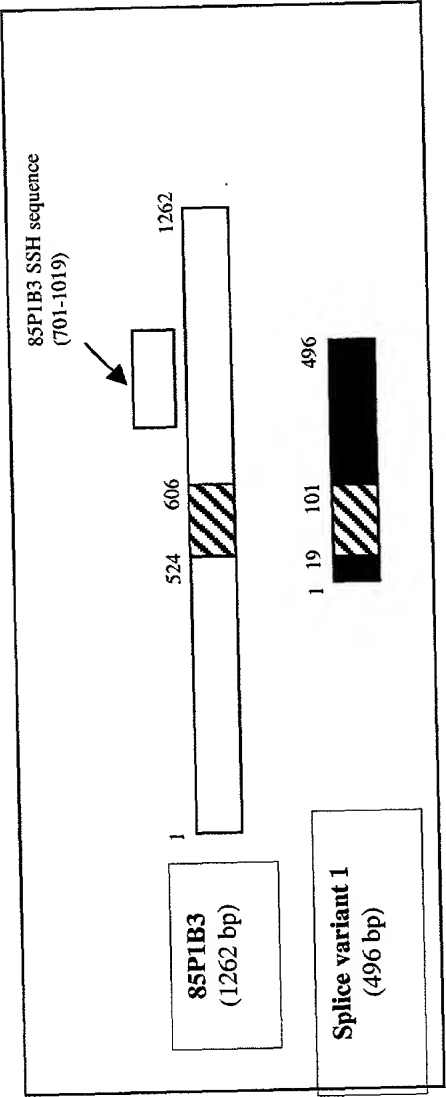


Figure 19.



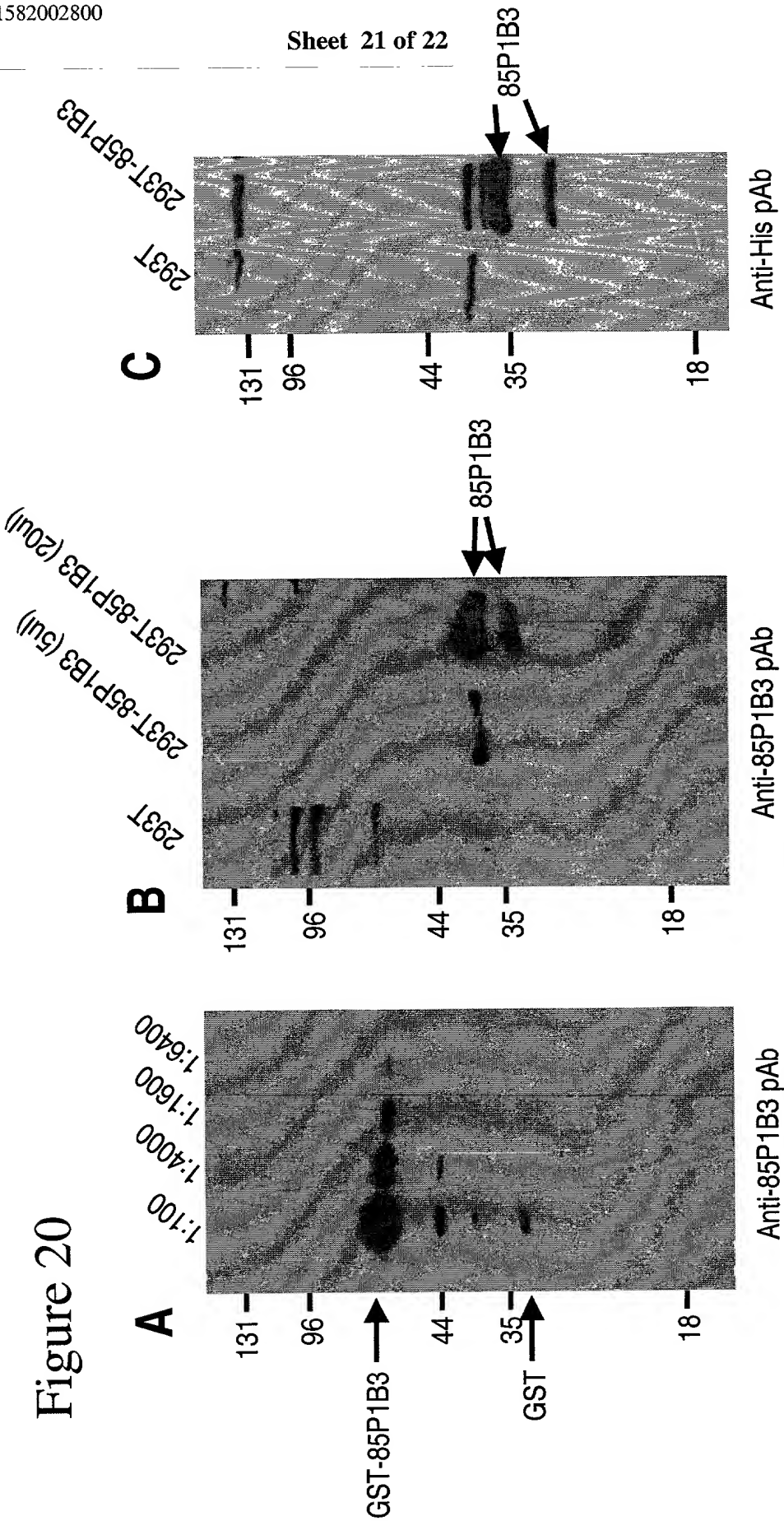


Fig. 21A

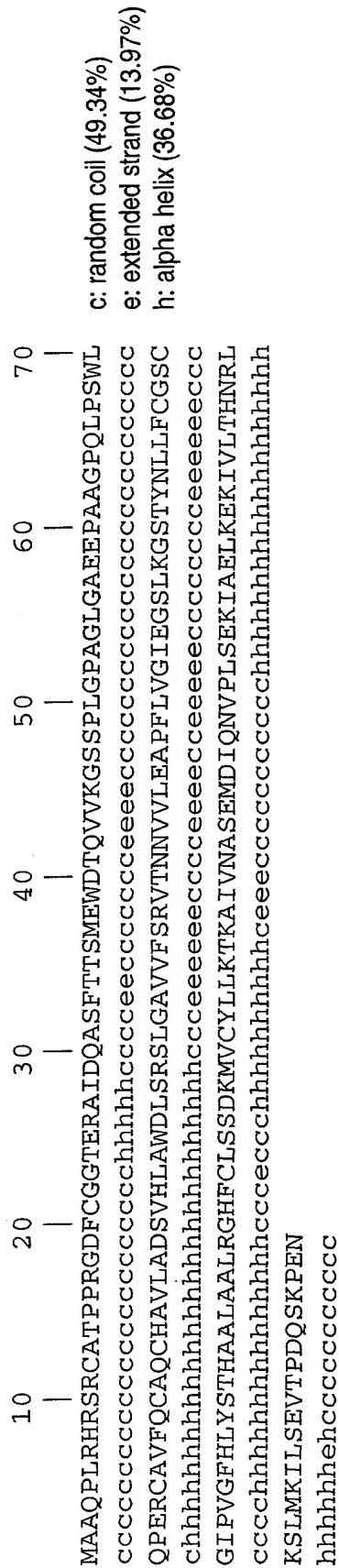
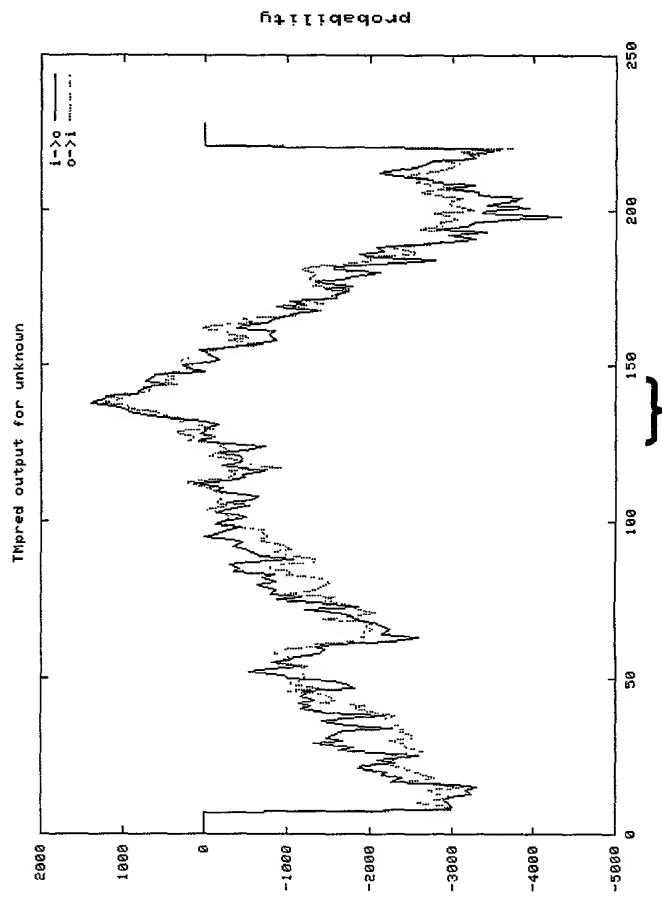
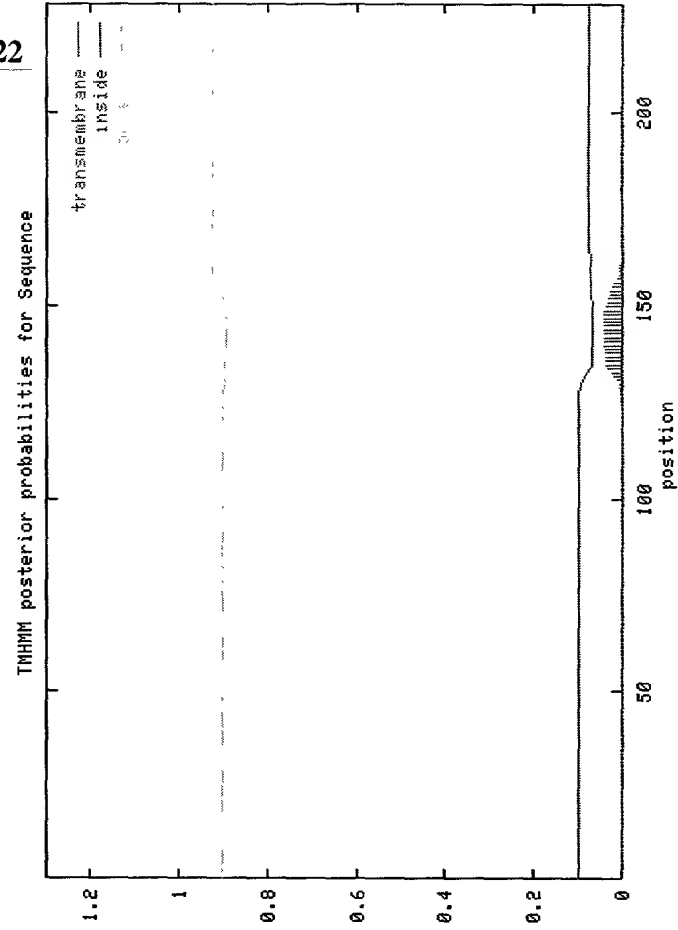


Fig. 21B



1 transmembrane from amino acids 129-149

Fig. 21C



No transmembrane domains, soluble protein